Equivalent (6)

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U1S S1334

(56) Documents Cited
EP 0589636 A1 EP 0317286 A2 WO 93/25912 A1
WO 93/13400 A2 WO 92/05443 A1 US 5779907 A

(58) Field of Search
UK CL (Edition R) G1B BBN BCA BCF BCH
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(54) Abstract Title
Handling magnetic beads during assays

(57) Device for automated handling and separation of magnetic beads or spheres during assay procedures comprises a multipipette arrangement 1, a multicavity plate typically a microtitre plate 2, magnetic rods 4 and plate 3 and a handling mechanism(not shown). Utility is in purification of RNA/DNA products, solid phase sequencing, cell separation, mRNA isolation, RNA/DNA hybridisation and ELISA type assays. Higher throughput of microtitration plates is obtained.

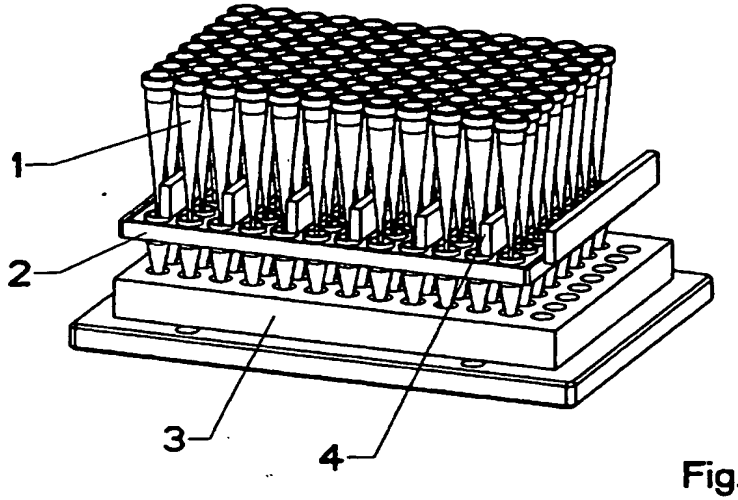

Fig. 1

GB 2 343 949 A

At least one drawing originally filed was informal and the print reproduced here is taken from a later filed formal copy.

EUROPEAN PATENT OFFICE

Patent Abstracts of Japan

PUBLICATION NUMBER : 63016884
PUBLICATION DATE : 23-01-88

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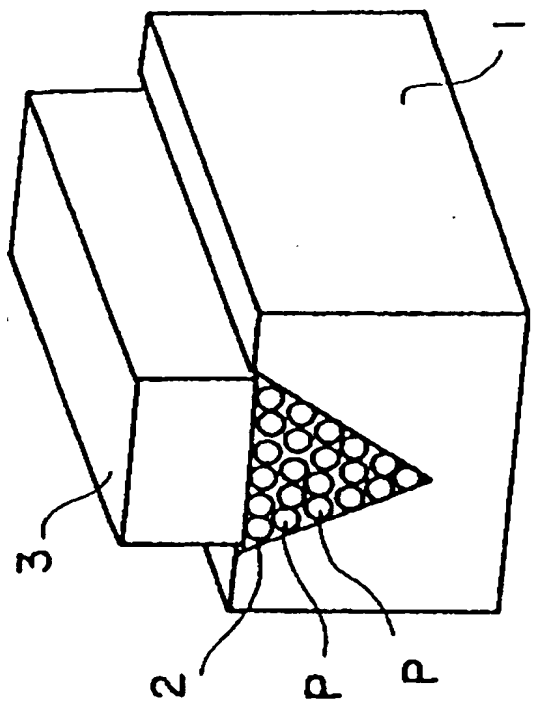
APPLICATION NUMBER : 61160607

APPLICANT : NITSUKOOSHI KK;

INVENTOR : MONZEN KAZUYUKI;

INT.CL. : B23K 20/00 B21D 47/00 B23K 1/00

TITLE : MANUFACTURE OF HONEYCOMB STRUCTURE



ABSTRACT : PURPOSE: To make a production efficient by subjecting metal made pipes having the same diameter and thickness to a closest packing into a jig in the prescribed number of pieces and pressing them by heating at ≤ the melting point of the metal and ≥ the diffusion temp. under a hydrogen or inert gas atmosphere.

CONSTITUTION: The pipe P of an iron base metal, Ni base metal, Al metal, copper or titanium metal in ≤ 1mm thickness and ≤ 1/10 of the diameter is subjected to a closest packing into a jig 1 in seven pieces as the minimum composition unit. A honeycomb structure is obtd. by pressing it by heating at ≤ the melting point and ≥ the diffusion temp. of the metal under a hydrogen or inert gas atmosphere. With this method, the product can be manufactured effectively and easily.

FJS/09/15

(3)

XP002916301

P.D. 28-10-97

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1398

Microsphere-based assays for genome analysis using flow cytometry.

J. P. Nolan, H. Cai, K. Kommander, and P. S. White (Intro. by: Larry Deaven). Los Alamos National Laboratory, Los Alamos, NM

Large scale sequence and single-base polymorphism analysis of the human genome requires robust and sensitive screening methods which are amenable to automation and high throughput analysis. We are developing a suite of microsphere-based approaches employing fluorescence detection by flow cytometry to screen for and analyze single base polymorphisms. One approach being developed for polymorphism detection is to immobilize on microspheres proteins which recognize specific DNA structures. When a fluorescently labeled DNA molecule binds to the immobilized protein, the binding can be measured by flow cytometry. An example is the binding of the mutS protein to single base mismatches formed when heteroduplex DNA hybridizes. To analyze nucleotide base frequencies at a polymorphic site, we are developing an approach based on minisequencing in which immobilized primers designed to interrogate a specific site are used to bind the region of interest in an unknown sample. The primers are then extended by polymerase using fluorescent ddNTPs and flow cytometry is used to read the frequency of each differently colored base. Apart from the advantages of sensitivity and low sample consumption, the flow cytometric approaches have the advantages of the potential for multiplexed analysis using different color or size beads and automated sample handling. Multiplexed analysis could enabled simutaneous analysis of base frequencies at dozens of different loci, which combined with automated sample handling could provide a powerful tool for high throughput screening of single base polymorphisms. Supported by NIH and DOE.